

IN THE CLAIMS:

Please cancel claims 1-18 without prejudice and add new claims 19-36.

19. A method of transforming trees to modify fibre characteristics in trees, the method comprising stably incorporating into the plant genome a chimaeric gene comprising a promoter and a nucleic acid sequence encoding an expansin capable of modifying at least one of: fibre cell wall extension, tree height or internode length, or a combination thereof; said nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-6, the cucumber expansin sequence cucumber Ex29 (GenBank Accession No. U30382), parts thereof, sequences substantially similar thereto and having the same function, and combinations thereof; and regenerating a tree having an altered genome.

20. A method according to Claim 19, wherein said nucleic acid sequence is derived from *Eucalyptus* or cucumber.

21. A method according to Claim 19, wherein said nucleic acid sequence is an mRNA, a cDNA sequence or a genomic DNA.

22. A method according to Claim 19, wherein said nucleic acid sequence, or part thereof, is arranged in a normal reading frame direction or in a reverse reading frame direction.

23. A method according to Claim 22, wherein said nucleic acid, or part thereof, is arranged in the normal reading frame direction and a decrease in internode length and/or plant height is achieved.

24. A nucleic acid sequence encoding a gene capable of modifying at least one of: fibre cell wall extension, tree height or internode length, or a combination thereof; wherein the nucleic acid

sequence is selected from the group consisting of SEQ ID NOs: 1-6, parts thereof, sequences substantially similar thereto and having the same function, and combinations thereof.

25. A chimaeric gene comprising a nucleic acid sequence according to claim 24 and a promoter.

26. A chimaeric gene according to Claim 25, wherein said chimaeric gene further comprises a terminator.

27. A chimaeric gene according to Claim 25, wherein said chimaeric gene comprises said nucleic acid sequence as said nucleic acid sequence exists in nature, with or without introns, complete with endogenous promoter, terminator, and other regulatory sequences.

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28. A chimaeric gene according to Claim 25, wherein said chimaeric gene comprises said nucleic acid sequence, with or without introns, combined with a heterologous promoter, terminator and/or other regulatory sequences.

29. A chimaeric gene according to Claim 25, wherein said promoter is selected from the group consisting of the cauliflower mosaic virus 35S promoter (CaMV35S), the cauliflower mosaic virus 19S promoter (CaMV19S), the nopaline synthase promoter, the *rolC*, patatin or *petE* promoters, the AlcR/AlcS promoter and a fibre-related promoter.

30. A chimaeric gene according to Claim 25, wherein said nucleic acid sequence, or part thereof, is arranged in a normal reading frame direction or in a reverse reading frame direction.

31. A method according to Claim 19, wherein said chimaeric gene is a chimaeric gene as claimed in Claims 25-30.

32. A tree comprising a chimaeric gene of Claims 25-30.

33. A plant cell comprising a chimaeric gene of Claims 25-30.

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cont* 34. A tree transformed according to the method of Claims 19-23 or 31.

35. A tree as claimed in Claim 34, said tree being a eucalypt, aspen, pine or larch.

36. A seed of a tree transformed according to the method of Claims 19-23 or 31.
